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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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EXAMINER	
PRIEBE,S	
ART UNIT	**PAPER NUMBER**
1632	19

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Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Advisory Action

Application No.	Applicant(s)
09/206,040	Byrum et al.
Examiner	**Group Art Unit**
Scott D. Priebe, Ph.D.	1632

THE PERIOD FOR RESPONSE: [check only a) or b)]

a) ☐ expires _____ months from the mailing date of the final rejection.

b) ☐ expires either three months from the mailing date of the final rejection, or on the mailing date of this Advisory Action, whichever is later. In no event, however, will the statutory period for the response expire later than six months from the date of the final rejection.

Any extension of time must be obtained by filing a petition under 37 CFR 1.136(a), the proposed response and the appropriate fee. The date on which the response, the petition, and the fee have been filed is the date of the response and also the date for the purposes of determining the period of extension and the corresponding amount of the fee. Any extension fee pursuant to 37 CFR 1.17 will be calculated from the date of the originally set shortened statutory period for response or as set forth in b) above.

☒ Appellant's Brief is due two months from the date of the Notice of Appeal filed on *Sep 22, 2000* (or within any period for response set forth above, whichever is later). See 37 CFR 1.191(d) and 37 CFR 1.192(a).

Applicant's response to the final rejection, filed on *ug 22 & Sep 22, 200* has been considered with the following effect, but is NOT deemed to place the application in condition for allowance:

☒ The proposed amendment(s):

☒ will be entered upon filing of a Notice of Appeal and an Appeal Brief.

☐ will not be entered because:

☐ they raise new issues that would require further consideration and/or search. (See note below).

☐ they raise the issue of new matter. (See note below).

☐ they are not deemed to place the application in better form for appeal by materially reducing or simplifying the issues for appeal.

☐ they present additional claims without cancelling a corresponding number of finally rejected claims.

NOTE: _____

☒ Applicant's response has overcome the following rejection(s):
The rejection of claims 1-3 under 35 USC 112, 2nd para. and of claims 1 and 3 under 35 USC 102(b).

☐ Newly proposed or amended claims _____ would be allowable if submitted in a separate, timely filed amendment cancelling the non-allowable claims.

☒ The affidavit, exhibit or request for reconsideration has been considered but does NOT place the application in condition for allowance because:
See attachment

☐ The affidavit or exhibit will NOT be considered because it is not directed SOLELY to issues which were newly raised by the Examiner in the final rejection.

☒ For purposes of Appeal, the status of the claims is as follows (see attached written explanation, if any):

Claims allowed: *none*

Claims objected to: *none*

Claims rejected: *1-3*

☐ The proposed drawing correction filed on _____ ☐has ☐has not been approved by the Examiner.

☐ Note the attached Information Disclosure Statement(s), PTO-1449, Paper No(s). _____ .

☐ Other

SCOTT D. PRIEBE, PH.D.
PRIMARY EXAMINER
ART UNIT 1632

Advisory Action (cont.)

General comment regarding the arguments in section 1 traversing the related rejections under 35 USC 101 and 112, first para.

The Wiegand declaration presents further characterization of the claimed nucleic molecules that was not included in the original specification. Since this new information was not disclosed in the original specification, it could not be included in any evaluation of utility for the claimed invention. This situation is similar to that of *In re Kirk,* 376 F.2d 936, 153 USPQ 48, 52 (CCPA 1967), where the Appellant had unsuccessfully attempted to establish a utility for a claimed invention by means of an affidavit describing experimental results, absent from the original specification, supporting a specific and substantial utility that had also not been disclosed in the original specification. The disclosure must have met the requirements of 35 USC 101 and 112, first paragraph at the time the application was filed.

Response to arguments in sections 1.a.1 and 1.a.2.

The arguments in Section 1.a.1 and 1.a.2 of the after-final response are directed to Examiner's arguments at pages 3-6 in the final Office action. In the final Office action, the Examiner's arguments were directed to Applicant's unsupported assertion in the response of 7/6/99 that merely because one obtains an EST, that the existence of the EST alone (i.e. without further characterization) is *proof* that the template from which it was made is a mRNA with biological function *in vivo*, and that this characteristic of an EST alone suffices to meet the utility

requirement. The evidence provided in the final Office action contradicts the unsupported assertion that the existence of an EST alone is *proof* that the template from which it was made is an mRNA that has biological function *in vivo*.

The primary issue raised in the final Office action on this issue is obscured by the side issues regarding whether existence of an EST alone is sufficient to establish by a preponderance of evidence that the corresponding mRNA exists *in vivo* and has biological function *in vivo*. The main issue (see final Office action, para. bridging pages 3-4) is whether only the knowledge that an EST corresponds to a functional gene is sufficient to confer a specific and substantial utility. It remains that there is no disclosure of a utility that is specific to the claimed nucleic acid molecules based on mRNA or gene function, other than as an object of further experimentation to determine the function of the corresponding gene. The use of the claimed nucleic molecules to determine the function of the corresponding mRNA constitutes further characterization of the claimed invention, which use does not meet the statutory requirement for a specific and substantial utility. Potential uses of the claimed nucleic acid molecules for assaying mRNA expression levels in tissues or for mapping, etc. discussed in subsequent sections do not require knowledge of the function of any protein encoded by mRNA.

With respect to the premise that the existence of the EST proves that the corresponding mRNA is functional *in vivo*, the methods used to obtain the claimed EST were known to produce artifactual sequences, for example, due to error prone DNA synthesis and formation of chimeric sequences during PCR amplification, particularly if repetitive sequences are involved, and it was

known that a large fraction of the genomes of plants in general and soybean in particular are repetitive sequences. As stated in the Wiegand declaration (para. 8), PCR amplification is error prone and may generate chimeric and repeated DNA. It further states that generation of chimeric and repeated DNA is uncommon, but does not provide any evidence to support this statement. The evidence provided in the final Office action suggests that the frequency of such artifacts of PCR depend upon the specific reaction conditions used. The specification fails to provide sufficient detail on the PCR method employed in making the claimed EST or on any controls that were employed to ensure that the EST was not chimeric or did not contain repeated sequences. The Wiegand declaration (para. 16-18) provides evidence that SEQ ID NO: 1 does not include repetitive sequences and is not chimeric. However, this experimental characterization was not disclosed in the specification, so that while one now knows that the claimed nucleic acid molecule corresponds to a unique soybean sequence, one would not have had a reasonable basis to conclude that it corresponded to a unique sequence at the time the application was filed.

Second, the genomes of higher plants were known to contain pseudogenes, some of which are transcribed; pseudogenes do not express a biologically functional product. It is argued that the four prior art references, showing the existence of pseudogenes, supplied in the final Office action, are not pertinent since the Wiegand declaration shows that the claimed nucleic acid molecule hybridizes to an mRNA in soybean that is not derived from a mitochondrial mRNA (as were pseudogenes described in three of the references). However, it must be kept in mind that the identification of pseudogenes has been ancillary to studies carried out for other purposes. There

is no evidence that those skilled in the art had engaged in any efforts dedicated to determining the prevalence of pseudogenes in any genome. Therefore, based on the limited prior art available one can conclude that pseudogenes exist; and that any given cDNA, including the disclosed EST, may be derived from a transcribed pseudogene. However, the likelihood that any particular EST is derived from a pseudogene cannot be determined in the absence of further study to determine their prevalence in genomes, such as the soybean genome. The Wiegand declaration does not provide any evidence that the EST of the claimed nucleic acid molecules is not derived from the mRNA of a transcribed pseudogene. Thus, it is still hypothetical that the disclosed EST corresponds to a functional gene.

The evidence presented in the Wiegand declaration supports Applicant's hypothesis that the disclosed EST corresponds to a single mRNA and gene that is functional *in vivo*. However, Applicant has failed to provide evidence showing that such knowledge alone does any more than provide an invitation to experiment first to determine just what that function is, and to then identify potential specific, substantial and credible uses for the claimed nucleic acid molecule based on that as yet unknown function. The Supreme Court *(Brenner v. Manson*, 148 USPQ 689, 696 (US SupCt 1966)) has held:

> a patent is not a hunting license. It is not a reward for the search, but compensation for its successful conclusion. "[A] patent system must be related to the world of commerce rather than to the realm of philosophy.

Response to arguments in section 1.a.3.

It is argued that "the underlying biological value of the nucleic acid molecules", for which EST sequences are determined, is the basis for the perceived value in EST databases. It is also stated (referring to para. 6 of the Wiegand declaration) that the clones corresponding to the specific EST sequences are often transferred when the database access is sold; and that the databases are used to compare nucleotide sequences or to select appropriate clones "for further research" (Wiegand decl., para. 6). In response, the comparison of nucleotide sequence information does not involve nucleic acid molecules. It is not clear how the mental process used in comparing nucleotide sequence information is germane to the utility of the specific nucleic acid molecules claimed. The specification does not disclose any particular significance of the claimed nucleic acid molecules; and discloses no purpose, "real-world" benefit in readily apparent form for the claimed molecules, to be served by comparing an uncharacterized nucleotide sequence, such as the core sequence of the claimed nucleic acid molecules, to nucleotide sequences of other unspecified and uncharacterized nucleic acid molecules. Furthermore, using clones identified by comparing nucleotide sequence information for "further research" does not meet the utility requirement, since this use is research on the claimed invention. It is not research using the claimed invention to accomplish some other purpose that would specifically require the claimed nucleic acid molecules. Instead, such research is further experimentation on the material being claimed to identify or reasonably confirm a "real-world" use. The Wiegand declaration (para. 6) notes that commercial EST libraries are sold for two-hybrid analysis (tests protein-protein

interaction) and as expression arrays. However, while this might, potentially, provide a use for such a library, it does not provide a specific, substantial and credible use for an individual member of the library *per se*. The specification does not disclose that SEQ ID NO: 1 contains any protein coding sequence, nor is it clear how one would use such information even were it present.

It is further argued that the commercial success of the EST database industry is evidence of utility for ESTs in general, and, presumably by association, the claims directed to nucleic acid molecules comprising a specific EST. In response, the fact that someone is willing to pay for a database of sequence information from a collection of EST clones does not necessarily indicate that either a nucleic acid molecule comprising an individual EST or even a collection of EST clones meets the utility requirement under 35 USC 101. Copyrighted works have commercial value, but this value in itself does not make them useful within the meaning of 35 USC 101. No evidence has been provided that explains why purchasers consider the databases (and associated clones) valuable. No evidence has been provided that the clones, rather than information associated with the library, are the product valued by the purchasers, or more importantly that the separately claimed nucleic acid molecule would be so valued. It is noted that many commodities are bought and sold which are not subject matter for which patents are granted, for example books, magazines, gemstones, and real estate. Also, just because one can make money off of a fad item, such as a Pet Rock®, does not make the fad item useful.

In addition, as noted above, a library of many different ESTs may have utility because valuable information may be gleaned from the library as a whole. However, this does not mean

that any specific EST present in the library has utility, or will have utility. Such could only be determined once a particular member of the library were subjected to use testing. Applicant's argument suggests that the claimed nucleic acid molecule has utility because one of skill in the art may, in the future, develop a specific and substantial utility for it. However, such a utility for an isolated EST does not meet the statutory requirement, since such a utility is as an object of research in order to determine or reasonably confirm a potential substantial utility.

Response to arguments in section 1.b.

It is argued that the claimed nucleic acid molecules have "utility as tools, e.g. hybridization probes", similar to a novel microscope or cell-based drug screening assay. The use of a microscope is not limited to any particular sample, whereas the claimed nucleic acid molecule would be. It is argued that "the claimed nucleic acid molecules may be used to locate and measure nucleic acid molecules within a sample, cell or organism". While this may be true, the issue is - "To what end?". The only nucleic acid molecules that could be located or measured are nucleic acid molecules embraced by the claims. The only apparent purpose for such locating and measuring would be to further characterize the claimed invention to identify or establish a specific, substantial and credible utility.

A cell-based screening assay, for identification ligands to a receptor for example, would only meet the utility requirement if certain conditions were met. First, the specification would have to teach the parameters which can be measured to identify an appropriate ligand with

specific function determined by the assay itself. Second, the specification would have to teach some practical utility for at least one ligand identified by the assay, e.g. use as a drug. If the sole use for all of the ligands is in the assay itself, the assay would not meet the substantial utility requirement because no use other than a research "curiosity" would be present. In the instant case, however, the claimed nucleic acid molecule can only be used to identify a nucleic acid molecule complementary to itself, and the function of the complementary nucleic acid molecule is completely unknown as well. The specification fails to disclose any useful product that can be identified or made using the claimed nucleic acid molecules, as probes for example.

Response to arguments in section 1.c and 1.c.3.

In section 1.c, it is asserted that the final Office action at page 8 was inaccurate, that the specification did identify a "specific plant tissue" that expressed the mRNA corresponding to the disclosed EST. In response, "young seed pods" are not tissue, although they comprise tissues. The specification (page 24, para. 2) clearly indicates that the nucleic acid molecules were isolated from the pod and the seeds contained in the pod. The specification does not disclose which specific tissue(s) contained in the young seed pods expressed the mRNA; nor does it disclose what other soybean tissues, such as from adult plants, expressed the mRNA. As a result, the specification fails to teach whether or how the disclosure of the source material from which the EST of the claimed molecules was prepared would result in a discriminating probe that could be used for a specific, substantial and credible utility. The Wiegand declaration at paragraph 17 (but

not the specification) discloses that the mRNA is also expressed in one or more sprout tissues and in adult leaf tissue. While knowing that the claimed nucleic acid molecules are expressed in at least one tissue in seed pods, sprouts or adult tissue may be of scientific interest, it is not clear how this information confers a specific and substantial utility on the claimed nucleic acid molecules.

In section 1.c.3, it is asserted that it is routine to use "nucleic acids representing ESTs" "to study the expression of the corresponding genes". It is also asserted that knowing the conditions under which the claimed nucleic acid molecule is expressed and the levels of expression in certain tissues "is in itself useful", for example changes in expression of traits of interest under drought stress. However, the specification does not disclose a corresponding gene, nor does it disclose "conditions" under which the claimed nucleic acid molecule is expressed or not expressed, nor does it disclose any levels of expression of the claimed nucleic acid molecule in different tissues, nor does it disclose any "traits of interest" associated with expression of the claimed nucleic acid molecules.

These uses of the claimed nucleic acid molecules constitute only further characterization of the claimed invention, e.g. identifying tissue in which the corresponding mRNA is expressed, or identifying a trait associated with expression of the claimed nucleic acid molecules. The claimed product, when used in this manner, is merely an object of scientific inquiry. Such a use does not comply with the requirements of 35 USC 101.

Response to arguments in section 1.c.1.

It is argued that using the claimed nucleic acid molecules to determine the presence or absence of a polymorphism, and if polymorphisms are present, to identify and characterize them does not constitute "use testing". This utility is compared to using a biological assay to screen for chemicals which themselves may have no utility, and it is asserted that such a biological assay and the constituents of such an assay have utility. No legal support for the latter has been provided. If such an assay would only identify compounds that have no utility, then the assay would also have no utility. Such a fact situation is similar to a method for making compounds with no known utility or intermediate products used in such a method. Contrary to applicants assertion, the Courts have held that such methods and intermediate products do not meet the utility requirement, see *Brenner v. Manson*, 383 U.S. 519, 534-535, 148 USPQ 689, 696 (US SupCt., 1966) and *In re Kirk*, 376 F.2d 936, 153 USPQ 48, 56 (CCPA 1967).

Paragraph 2 of section 1.c.1 mischaracterizes the arguments in the final Office action (pages 9-10). The final Office action describes the experiments needed to be carried out by the skilled artisan to determine *if* and *how* methods involving the analysis of polymorphisms could be practiced with the claimed invention. As explained, one would first have to determine whether the claimed nucleic acids could, in fact, be used to detect a polymorphism. Clearly, if the claimed nucleic acid molecule could not detect a polymorphism, then it could not be used for any method involving analysis of polymorphisms. That one skilled in the art would have to engage in such activity constitutes research on the claimed invention directed at determining a use for the claimed

nucleic acid molecule, i.e. "use testing". The fact that the Wiegand declaration shows that the nucleic acid molecules do detect polymorphisms, albeit between two different species of *Glycine*, does not alter the simple, incontrovertible fact that such an experiment was necessary before one could begin to take the next step in determining how to exploit this characteristic of the claimed invention for a practical utility. Simply because the claimed invention can be used in experiments on the claimed invention, does not mean that such use meets the utility requirement.

With respect to the findings in the Wiegand declaration (paras. 22-23), the specification does not describe identifying polymorphisms between species, nor does it describe any utility for doing so. Rather the specification (pages 27-29, particularly at page 28, full para. 4 to the para. bridging pages 28-29) describes analyzing polymorphisms within the same species. As defined in the specification, "a "polymorphism" is a variation or difference in the sequence of the gene or its flanking regions that arises in some of the members of a species". Thus the specification, as originally filed, does not contemplate the use of distinguishing between two different *Glycine* species based on polymorphisms, which were discovered after the application was filed.

Response to arguments in section 1.c.2.

With respect to the use of the claimed nucleic acid molecules for physical or genetic mapping, it is asserted that the Examiner was incorrect in stating that the first step in determining the map location of the claimed nucleic acid molecules would be to determine the copy number. First, this is a misstatement of the Examiner's position, which was that one would have to first

determine whether the claimed nucleic acid molecule contained repeated sequences located in different positions in the soybean genome, and that if it did, it was unclear how the claimed nucleic acid molecule could be used for mapping. Second, there is no explanation as to why the Examiner's position is incorrect. It is noted that the Wiegand declaration (e.g. paragraphs 22 and 23) provides evidence, not disclosed in the instant specification, that the claimed nucleic acid molecule is present in only a single copy in the haploid soybean genome, i.e. it does not contain repeated sequences located in different locations. Thus, while the physical or genetic map location of the claimed nucleic acid molecule in the soybean genome is still unknown, Wiegand has in fact performed the first step suggested by the Examiner of determining whether the claimed nucleic acid molecule was present in a single location in the genome.

Applicant asserts that without knowing more than the sequence of the claimed nucleic acid molecule, it can be used to determine a physical or genetic map location (presumably for the claimed nucleic acid molecule), and thus one can use the claimed invention - citing the Wiegand declaration at paragraph 12. However, no explanation is given as to how it is possible to determine a physical or genetic map location knowing only the sequence of the claimed nucleic acid molecule. Paragraph 12 of the Wiegand declaration merely asserts that the disclosed EST can be used to detect polymorphisms, which in turn are useful as molecular markers, and that molecular markers are useful to plant breeders. The response mentions general activities for which molecular markers have been used. While some specific molecular markers have been used for these purposes, this is a general utility for the class of nucleic acid molecular markers, wherein

specific molecular markers have been identified for certain traits of interest to plant breeders. The specification does not disclose any specific traits or genes for which the claimed nucleic acid molecule could be used as a molecular marker, i.e. the specification fails to disclose a specific utility for the claimed invention with respect to these activities. The specification also fails to disclose any molecular basis for using the claimed nucleic acid molecules as molecular markers since it discloses no polymorphisms that could be detected. Furthermore, using the claimed nucleic acid molecule to map its location merely constitutes further characterization of the claimed invention. Simply because the claimed invention can be used in experiments on the claimed invention itself, does not mean that such use meets the specific and substantial utility requirement - the specification does not disclose any "real-world" context for using the claimed nucleic acid molecules based on the resulting information.

Response to arguments in section 1.c.4.

With respect to using the claimed nucleic acid molecules to make probes and primers to identify other specific nucleic acids, Applicant states that the specification teaches that such probes and primers could be used to isolate nucleic acid molecules of other plant species. However, the specification fails to disclose any such nucleic acid molecules from other plant species. Nor does the specification teach what use these nucleic acid molecules of other plant species would have. Any uncharacterized nucleic acid molecule from a species of organism can be used in this manner, thus such a utility is not specific to the claimed invention, and since the

specification discloses no biological function or any use for any gene corresponding to the claimed nucleic acid molecule, any such nucleic acid molecules of other plant species would also lack substantial utility - the artisan would first have to experiment to determine a specific, substantial and credible use for any such nucleic acid molecules isolated.

It is argued that the claimed nucleic acid molecule would have utility for initiating a chromosomal walk in order to isolate the promoter for the gene corresponding to the claimed nucleic acid molecule, which would be useful for expression in young pods of proteins, such as proteins providing disease resistance. In response, using a nucleic acid molecule as a starting point for a chromosome walk is a general characteristic common to nucleic acid molecules isolated from any organism, e.g. cDNA or genomic DNA, this is a utility not specific to the claimed polynucleotide. Further, the specification does not disclose any particular reason why one should initiate a chromosome walk at the unknown chromosomal location corresponding to the claimed nucleic acid molecule. With respect to the corresponding promoter, the specification does not disclose any distinguishing characteristics of this promoter nor does it disclose the location of this promoter relative to the chromosomal location corresponding to the claimed nucleic acid molecule, which is also unknown. Since the claimed nucleic acid molecule is presumed to be chromosomal in origin, one would expect that a chromosome walk from the corresponding chromosomal location would eventually result in identification of putative promoters, based on sequence analysis, from the same gene or from genes in adjacent chromosomal regions. The specification does not teach how one would determine whether any

such hypothetical promoter would be that corresponding to the gene of the claimed nucleic acid molecule. With respect to the hypothetical use for the corresponding promoter for gene expression of a protein providing disease resistance in young pods, the specification does not describe such a use, or that such would have been well established. Also, as shown by the Wiegand declaration (Exhibit B), the gene corresponding to the claimed nucleic acid molecule is expressed in sprouts and adult leaves, it is not restricted to expression in young pods.

Response to arguments in section 1.c.5.

With respect to the use of the claimed nucleic acid molecule to identify antisense inhibitors, the Office action of March 22, 2000 did not say that it was not possible to identify antisense molecules; the action described what would have been required to do so. The action simply pointed out that the specification did not disclose: a) that the claimed nucleic acid molecule itself had antisense activity, b) an assay for detection of antisense activity, and c) any utility for such an antisense molecule even if one were known.

Response to arguments in section 2.

The additional grounds for a lack of enablement apply to claimed nucleic acid molecules that comprise SEQ ID NO: 1 and one or more unspecified components, such as additional, unspecified nucleic acid sequences. It is asserted that the rejection should be withdrawn because it only takes into account the use of the nucleic acid molecules comprising SEQ ID NO: 1 as

probes or primers and does not take into account any of the other disclosed utilities. In response, the specification does not disclose any utilities for the claimed nucleic acid molecules that does not involve using them as a probe or primer.

It is argued that one skilled in the art would be able to rely on their own knowledge of nucleic acid hybridization and polymerase chain reaction in designing probes and primers for a particular purpose, since the parameters for such methods are well characterized. For example, it is acknowledged (citing para. 13 of the Wiegand declaration) that one skilled in the art would know that addition of soybean sequences would prevent efficient use of such a combined sequence as a hybridization probe. However, the claim embraces just such embodiments and the specification fails to teach how to use such embodiments. Furthermore, that one skilled in the art would avoid combining other soybean sequences to SEQ ID NO: 1 presupposes that one would know whether any arbitrarily chosen nucleic acid sequence was or was not soybean nucleic acid or would or would not cross-hybridize with soybean nucleic acid. One cannot predict this without knowing the identity of all soybean nucleic acid sequences. Make-and-test experimentation would be required to determine whether any arbitrarily chosen sequence would hybridize or pair with soybean sequences other than the desired target.

The response goes on to summarize a *Wands* analysis of the claims presented in the response of July 6, 1999. This analysis would be effective if claims 1 and 3 were limited to nucleic acid molecules which either consist of SEQ ID NO: 1 or comprised additional sequences that would not interfere with hybridization or PCR amplification of a target sequence comprising

SEQ ID NO: 1 and were conventionally added to probes and primers. The Examiner acknowledges that a range of small nucleic acid sequences are routinely added to nucleic acids to be used as probes or primers, such as primer binding sequences for nested PCR reactions and binding sites for capture probes for amplifying hybridization signals, or linkers and adapters for cloning and vector backbones for maintenance and production of a probe.

However, the claims are not limited to nucleic acid molecules consisting of SEQ ID NO: 1 linked to nucleic acids that are conventionally added to a core probe sequence, such as SEQ ID NO: 1. Rather, the claims also embrace a far larger number of nucleic acid molecules that comprise sequences that are not conventional for hybridization and PCR amplification and that would interfere with detection of a target nucleic acid comprising SEQ ID NO: 1. It is this much larger subgenus embraced by claims 1 and 3 that the specification fails to describe how to use. (Note that the transitional phrase "consisting essentially of" excludes only those elements affecting the basic and novel characteristic of the claimed invention. In the instant case, there is no clearly defined characteristic, and therefore, it is unclear what would be excluded. Therefore, in a practical sense claim 3 may be construed as using the open "comprising" transitional phrase as in claim 1.)

Response to arguments in section 3.

The issue is whether Applicant was in possession of the genus being claimed (claims 1 and 3). This genus is not restricted to any particular disclosed subgenus or species, such as vectors

comprising SEQ ID NO: 1 as an insert. The only nucleic acid molecule described by complete structure is the one consisting of SEQ ID NO: 1. The only nucleic acid molecules comprising or consisting essentially of SEQ ID NO: 1 described in the specification by other characteristics are generic vectors comprising SEQ ID NO: 1. While it is acknowledged that Applicant need not describe "every nuance" of the claimed invention, the written description must bear a reasonable correlation to that which is claimed. The disclosed subgenus and species embraced by the claims are not representative of the entire genus being claimed. The genus of nucleic acid molecules being claimed embraces any and every type of molecules that comprise SEQ ID NO: 1 and additional sequences of any size and sequence, not just vector backbones. Clearly, at the time of filing, Applicant was not in possession of all genes that contain the common EST fragment, which are embraced by the open-ended claims. The specification does not disclose what characteristics these additional sequences may or may not have that are consistent with the operability of the nucleic acid molecules as probes or primers for detection of SEQ ID NO: 1 in a target sequence, and all disclosed uses for the claimed nucleic acid molecules are fundamentally as probes or primers.

With respect to full length mRNAs, cDNAs and genomic sequences, one skilled in the art would reasonably conclude that the claims embrace these nucleic acid molecules, and the specification provides no physical (i.e. structural) characteristics of these molecules to distinguish them from other nucleic acid molecules comprising SEQ ID NO: 1 and no other indication that would suggest Applicant possessed them.

With respect to recitation in claim 3 of "consisting essentially of", the statement made in the Office action of March 22, 2000 at page 22, lines 10-14 was not intended to be a basis of the rejection. The statement was made to indicate why claims 1 and 3 were being treated the same in the rejection, i.e. that the specification provided no material limitation that would distinguish the subject matter of claims 1 and 3 from each other (see comment above). Applicant's statement indicates that claim 3 should exclude "ingredients that may materially affect" the use of the nucleic acid molecule as a probe. However, the specification does not describe what such ingredients might be. Also, this statement implies that claim 1 would include nucleic acid molecules that do comprise "ingredients that may materially affect" the use of the nucleic acid molecule as a probe or primer. The specification discloses no other use for the claimed nucleic acid molecules. Consequently, if there is subject matter embraced by claim 1 that is excluded by claim 3, there is no indication in the specification that Applicant was in possession of such subject matter and therefore of the broader genus of claim 1. (See *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398 (CA FC 1997) where disclosure of a rat insulin cDNA did not provide support for claims to mammalian insulin cDNA or human insulin cDNA.)

Certain papers related to this application may be submitted to Art Unit 1632 by facsimile transmission. The FAX number is (703) 308-4242 or 305-3014. The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 CFR 1.6(d)). NOTE: If applicant *does* submit a paper by FAX, the original copy should be retained by applicant or applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED, so as to avoid the processing of duplicate papers in the Office.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Scott D. Priebe whose telephone number is (703) 308-7310. The examiner can normally be reached on Monday through Friday from 8 AM to 4 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Karen M. Hauda, can be reached on (703) 305-6608.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Scott D. Priebe

Scott D. Priebe, Ph.D.
Primary Examiner
Technology Center 1600
Art Unit 1632